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TECH CENTER 1600/2900

1600

RAW SEQUENCE LISTING

DATE: 05/28/2003

PATENT APPLICATION: US/09/780,532A

TIME: 14:51:41

Input Set : A:\WYETH569.txt

Output Set: N:\CRF4\05282003\I780532A.raw

3 <110> APPLICANT: Wood, Clive
 4 Chaudhary, Divya
 5 Long, Andrew
 6 Genetics Institute, Inc.
 8 <120> TITLE OF INVENTION: TRADE MOLECULES, AND USES RELATED THERETO
 10 <130> FILE REFERENCE: 22058-569
 12 <140> CURRENT APPLICATION NUMBER: 09/780,532A
 13 <141> CURRENT FILING DATE: 2001-02-09
 15 <150> PRIOR APPLICATION NUMBER: 60/181,922
 16 <151> PRIOR FILING DATE: 2000-02-11
 18 <150> PRIOR APPLICATION NUMBER: 60/182,148
 19 <151> PRIOR FILING DATE: 2000-02-14
 21 <160> NUMBER OF SEQ ID NOS: 24
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1660
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(1251)
 34 <400> SEQUENCE: 1

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37	1 5 10 15	
39	tta gta tta cta ggc tat ttg tca tgt aaa gtg act tgt gaa tca gga	96
40	Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly	
41	20 25 30	
43	gac tgt aga cag caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc	144
44	Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro	
45	35 40 45	
47	tgc aac cag tgt ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc	192
48	Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe	
49	50 55 60	
51	ggc tat ggg gag gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc	240
52	Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe	
53	65 70 75 80	
55	aag gag gac tgg ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca	288
56	Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala	
57	85 90 95	
59	gtg gtg aac cgc ttt cag aag gca aat tgt tca gcc acc agt gat gcc	336
60	Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala	
61	100 105 110	

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63 atc tgc ggg gac tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc 384
64 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
65      115      120      125
67 ggc ttt caa gac atg gag tgt gtg cct tgt gga gac cct cct cct cct 432
68 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
69      130      135      140
71 tac gaa ccg cac tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc 480
72 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
73 145      150      155      160
75 acg gcc tcc agc cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc 528
76 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
77      165      170      175
79 gct ctg gcc acc gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat 576
80 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
81      180      185      190
83 tgt aag aga cag ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca 624
84 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
85      195      200      205
87 cag gac att cag tac aac ggc tct gag ctg tcg tgt ttt gac aga cct 672
88 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Phe Asp Arg Pro
89      210      215      220
91 cag ctc cac gaa tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac 720
92 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
93 225      230      235      240
95 tca gtg cag acc tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt 768
96 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
97      245      250      255
99 gag gag gcc tgc agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat 816
100 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
101      260      265      270
103 tct gca gcc agt ctt cag gca aga aac gca ggc cca gcc ggg gag atg 864
104 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
105      275      280      285
107 gtg ccg act ttc ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt 912
108 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
109      290      295      300
111 tca gat gcc tgg cct ctg atg cag aat ccc atg ggt ggt gac aac atc 960
112 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
113 305      310      315      320
115 tct ttt tgt gac tct tat cct gaa ctc act gga gaa gac att cat tct 1008
116 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
117      325      330      335
119 ctc aat cca gaa ctt gaa agc tca acg tct ttg gat tca aat agc agt 1056
120 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
121      340      345      350
123 caa gat ttg gtt ggt ggg gct gtt cca gtc cag tct cat tct gaa aac 1104
124 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
125      355      360      365
127 ttt aca gca gct act gat tta tct aga tat aac aac aca ctg gta gaa 1152

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128 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
129      370      375      380
131 tca gca tca act cag gat gca cta act atg aga agc cag cta gat cag 1200
132 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
133 385      390      395      400
135 gag agt ggc gct atc atc cac cca gcc act cag acg tcc ctc cag gaa 1248
136 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu
137      405      410      415
139 gct taaagaacct gcttctttct gcagtagaag cgtgtgctgg aacccaaaga 1301
140 Ala
142 gtactccttt gttaggctta tggactgagc agtctggacc ttgcatggct tctggggcaa 1361
144 aatgaatct gaaccaaact gacggcattt gaagcctttc agccagttgc ttctgagcca 1421
146 gaccagctgt aagctgaaac ctcaatgaat aacaagaaaa gactccaggc cgactcatga 1481
148 tactctgcat ttttcctaca tgagaagctt ctctgccaca aaagtgactt caaagacgga 1541
150 tgggttgagc tggcagccta tgagattgtg gacatataac aagaaacaga aatgccctca 1601
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156 <211> LENGTH: 417
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 2
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164 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly
165      20      25      30
167 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
168      35      40      45
170 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
171      50      55      60
173 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
174 65      70      75      80
176 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
177      85      90      95
179 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
180      100     105     110
182 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
183      115     120     125
185 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
186      130     135     140
188 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
189 145     150     155     160
191 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
192      165     170     175
194 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
195      180     185     190
197 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
198      195     200     205
200 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Phe Asp Arg Pro
201      210     215     220

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203 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
204 225                230                235                240
206 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
207                245                250                255
209 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
210                260                265                270
212 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
213                275                280                285
215 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
216                290                295                300
218 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
219 305                310                315                320
221 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
222                325                330                335
224 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
225                340                345                350
227 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
228                355                360                365
230 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
231                370                375                380
233 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
234 385                390                395                400
236 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu
237                405                410                415
239 Ala
243 <210> SEQ ID NO: 3
244 <211> LENGTH: 1325
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens
248 <220> FEATURE:
249 <221> NAME/KEY: CDS
250 <222> LOCATION: (1)..(1269)
252 <400> SEQUENCE: 3
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257 tta gta tta cta ggc tat ttg tca tgt aaa gtg act tgt gaa aca gga      96
258 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly
259                20                25                30
261 gac tgt aga cag caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc      144
262 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
263                35                40                45
265 tgc aac cag tgt ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc      192
266 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
267                50                55                60
269 ggc tat ggg gag gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc      240
270 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
271 65                70                75                80
273 aag gag gac tgg ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca      288

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274	Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala	
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277	gtg	gtg	aac	cgc	ttt	cag	aag	gca	aat	tgt	tca	gcc	acc	agt	gat	gcc	336
278	Val	Val	Asn	Arg	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	
279					100					105					110		
281	atc	tgc	ggg	gac	tgc	ttg	cca	gga	ttt	tat	agg	aag	acg	aaa	ctt	gtc	384
282	Ile	Cys	Gly	Asp	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	
283					115					120					125		
285	ggc	ttt	caa	gac	atg	gag	tgt	gtg	cct	tgt	gga	gac	cct	cct	cct	cct	432
286	Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	
287					130					135					140		
289	tac	gaa	ccg	cac	tgt	gcc	agc	aag	gtc	aac	ctc	gtg	aag	atc	gcg	tcc	480
290	Tyr	Glu	Pro	His	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	
291	145					150					155					160	
293	acg	gcc	tcc	agc	cca	cgg	gac	acg	gcg	ctg	gct	gcc	gtt	atc	tgc	agc	528
294	Thr	Ala	Ser	Ser	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	
295					165					170					175		
297	gct	ctg	gcc	acc	gtc	ctg	ctg	gcc	ctg	ctc	atc	ctc	tgt	gtc	atc	tat	576
298	Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	
299					180					185					190		
301	tgt	aag	aga	cag	ttt	atg	gag	aag	aaa	ccc	agc	tgg	tct	ctg	cgg	tca	624
302	Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	
303					195					200					205		
305	cag	gac	att	cag	tac	aac	ggc	tct	gag	ctg	tcg	tgt	ctt	gac	aga	cct	672
306	Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Leu	Asp	Arg	Pro	
307					210					215					220		
309	cag	ctc	cac	gaa	tat	gcc	cac	aga	gcc	tgc	tgc	cag	tgc	cgc	cgt	gac	720
310	Gln	Leu	His	Glu	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	
311	225					230					235					240	
313	tca	gtg	cag	acc	tgc	ggg	ccg	gtg	cgc	ttg	ctc	cca	tcc	atg	tgc	tgt	768
314	Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	
315					245					250					255		
317	gag	gag	gcc	tgc	agc	ccc	aac	ccg	gcg	act	ctt	ggg	tgt	ggg	gtg	cat	816
318	Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	
319					260					265					270		
321	tct	gca	gcc	agt	ctt	cag	gca	aga	aac	gca	ggc	cca	gcc	ggg	gag	atg	864
322	Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	
323					275					280					285		
325	gtg	ccg	act	ttc	ttc	gga	tcc	ctc	acg	cag	tcc	atc	tgt	ggc	gag	ttt	912
326	Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	
327					290					295					300		
329	tca	gat	gcc	tgg	cct	ctg	atg	cag	aat	ccc	atg	ggg	ggg	gac	aac	atc	960
330	Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	
331	305					310					315					320	
333	tct	ttt	tgt	gac	tct	tat	cct	gaa	ctc	gct	gga	gaa	gac	att	cat	tct	1008
334	Ser	Phe	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Ala	Gly	Glu	Asp	Ile	His	Ser	
335					325					330					335		
337	ctc	aat	cca	gaa	ctt	gaa	agc	tca	acg	tct	ttg	gat	tca	aat	agc	agt	1056
338	Leu	Asn	Pro	Glu	Leu	Glu	Ser	Ser	Thr	Ser	Leu	Asp	Ser	Asn	Ser	Ser	

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:24; Line(s) 1141

VERIFICATION SUMMARY

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